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September is National Mesothelioma awareness month! Mesothelioma is hard to detect, easily mis-diagnosed, and always fatal. Have your doctor check you for Mesothelioma or Pleural Mesothelioma today!

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0 1 2 3 4 5 6 7 8 9 A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

Generic term for a class of carotenes and their oxygenated derivatives (xanthophylls) consisting of 8 isoprenoid units joined so that the orientation of these units is reversed at the centre, placing the two central methyl groups in a 1,6 relationship in contrast to the 1,5 of the others. All carotenoids may be formally derived from the acyclic C₄₀H₅₆ structure (part IA, known as lycopene, of the accompanying group of structures) with its long central chain of conjugated double bonds by hydrogenation, dehydrogenation, oxidation, cyclization, or combinations of these. Included as carotenoids are some compounds arising from certain rearrangements or degradations of the carbon skeleton (structure IB), but not retinol and related C₂₀ compounds. The nine-carbon end-groups may be acyclic with 1,2 and 5,6 double bonds (as in structure IA) or cyclohexanes with a single double bond at 5,6 or 5,4, or cyclopentanes or aryl groups; these are now designated by Greek letter prefixes (illustrated in part II of the accompanying group of structures) preceding "carotene" (a and d, which are used in the trivial names alpha-carotene and d-carotene, are not used for that reason). Suffixes (-oic acid, -oate, -al, -one, -ol) indicate certain oxygen-containing groups (acid, ester, aldehyde, ketone, alcohol); all other substitutions appear as prefixes (alkoxy-, epoxy-, hydro-, etc.). The configuration about all double bonds is trans unless cis and locant numbers appear. The prefix retro- is used to indicate a shift of one position of all single and double bonds; apo- indicates shortening of the molecule. Many carotenoids have anticancer activities.

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Asbestos is a mineral widely used in the past because of its resistance to fire and heat. Loose asbestos fibers can lodge in the surrounding tissues of the lungs and cancerous tissues can develop into Pleural Mesothelioma. The disease may be treated with drugs like Alimta or Cisplatin, but it is essential for everyone to know the symptom and get tested for Mesothelioma.

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Polymers whose carbon skeletons consist in whole or in large part of isoprene units joined end to end; e.g., carotene, lycopene, vitamin A. Vitamins K and E and the coenzymes Q have isoprenoid side chains.

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-continued

Pro	Glu	Val	Leu	Val	Gln	Glu	Val	Ile	Asp	Gln	Leu	Lys	Ala	Trp	Gly
	275						280					285			
Gly	Glu	Thr	Thr	Ser	Val	Arg	Glu	Asn	Ser	Gly	Ile	Glu	Glu	Lys	Val
	290					295					300				
Val	Phe	Ser	Ile	Pro	Lys	Glu	Leu	Lys	Lys	His	Met	Gln	Ala		
305					310					315					

What is claimed is:

1. A method for the production of isoprenoid compounds comprising: contacting a transformed host cell under suitable growth conditions with an effective amount of a carbon source whereby an isoprenoid compound is produced, said transformed host cell comprising a nucleic acid molecules encoding SEQ ID NOs: ② under the control of suitable regulatory sequences.

2. A method according to claim 1 wherein the transformed host cell is selected from the group consisting of *Aspergillus*, *Trichoderma*, *Saccharomyces*, *Pichia*, *Candida*, *Hansenula*, *Salmonella*, *Bacillus*, *Acinetobacter*, *Rhodococcus*, *Streptomyces*, *Escherichia*, *Pseudomonas*, *Methylomonas*, *Methylobacter*, *Alcaligenes*, *Synechocystis*, *Anabaena*, *Thiobacillus*, *Methanobacterium* and *Klebsiella*.

3. A method according to claim 1 wherein said transformed host cell is a methanotrophic bacteria.

4. A method according to claim 3 wherein said methanotrophic bacteria:

- (a) grows on a C1 carbon substrate selected from the group consisting of methane and methanol; and
- (b) comprises a functional Embden-Meyerof carbon pathway, said pathway comprising a gene encoding a pyrophosphate dependent phosphofructokinase enzyme.

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5. A method according to claim 3 wherein the methanotrophic bacteria is selected from the group consisting of *Methylomonas*, *Methylobacter* and *Methanobacterium* and the carbon source is selected from the group consisting of methane and methanol.

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6. A method according to claim 4 wherein said methanotrophic bacteria is *Methylomonas* 16a ATCC PTA 2402.

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7. A method according to claim 1 wherein the transformed host cell is selected from the group consisting of soybean, rapeseed, sunflower, cotton, corn, tobacco, alfalfa, wheat, barley, oats, sorghum, rice, *Arabidopsis*, cruciferous vegetables, melons, carrots, celery, parsley, tomatoes, potatoes, strawberries, peanuts, grapes, grass seed crops, sugar beets, sugar cane, beans, peas, rye, flax, hardwood trees, softwood trees, and forage grasses.

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8. A method according to claim 1 wherein the carbon source is selected from the group consisting of monosaccharides, oligosaccharides, polysaccharides, carbon dioxide, methanol, methane, formaldehyde, formate, and carbon-containing amines.

30

* * * * *

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
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1	1215.5	61.2	396	2	E83188	1-deoxy-d-xylulose
2	1052.5	53.0	394	2	B82000	1-deoxy-D-xylulose
3	1045	52.6	398	2	E64741	yaeM protein - Esc
4	1044	52.6	398	2	G85501	1-deoxy-D-xylulose
5	1044	52.6	398	2	G90650	1-deoxy-D-xylulose
6	1040.5	52.4	394	2	A81229	1-deoxy-D-xylulose
7	1027	51.7	398	2	AF0529	1-deoxy-D-xylulose
8	1023	51.5	402	2	D82099	1-deoxy-D-xylulose
9	1020	51.4	398	2	AG0128	1-deoxy-D-xylulose
10	1007	50.7	397	2	A64014	conserved hypothet
11	941	47.4	396	2	H82728	1-deoxy-D-xylulose
12	892.5	45.0	394	2	S76331	hypothetical prote
13	891	44.9	398	2	F84957	1-deoxy-D-xylulose

Database : UniProt_02:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
1	1221.5	61.5	400	1	DXR_PSEPK	Q88mh4 pseudomonas
2	1215.5	61.2	396	1	DXR_PSEAE	Q9kgu6 pseudomonas
3	1201.5	60.5	396	1	DXR_PSESM	Q886n7 pseudomonas
4	1193.5	60.1	413	1	DXR_NITEU	Q82u01 nitrosomona
5	1113.5	56.1	394	1	DXR_CHRVO	Q7nvy8 chromobacte
6	1108.5	55.8	398	2	Q6FCG9	Q6fcg9 acinetobact
7	1091.5	55.0	393	1	DXR_RALSO	Q8xzi5 ralstonia s
8	1062	53.5	402	1	DXR_VIBVU	Q8dbf5 vibrio vuln
9	1060	53.4	402	1	DXR_VIBVY	Q7mig6 vibrio vuln
10	1052.5	53.0	394	1	DXR_NEIMA	Q9jx33 neisseria m
11	1047	52.7	401	1	DXR_VIBPA	Q87me3 vibrio para
12	1045	52.6	398	1	DXR_ECOLI	P45568 escherichia
13	1044	52.6	398	1	DXR_ECO57	Q8x8y1 escherichia
14	1042	52.5	405	1	DXR_PASMU	P57985 pasteurella
15	1041.5	52.5	396	1	DXR_SHEON	Q8egg9 shewanella
16	1040.5	52.4	394	1	DXR_NEIMB	Q9klg8 neisseria m

Database : A_Geneseq_23Sep04:*
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SUMMARIES

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2	1985	100.0	394	5	ABG61582	Abg61582 High grow
3	1985	100.0	394	5	AAU80326	Aau80326 Methylomo
4	1985	100.0	394	8	ADQ77216	Adq77216 Amino aci
5	1215.5	61.2	396	5	AAO21884	Aao21884 Isoprenoi
6	1215.5	61.2	617	7	ABO72367	Abo72367 Pseudomon
7	1114.5	56.1	398	6	ADA35912	Ada35912 Acinetoba
8	1053	53.0	399	7	ADF06177	Adf06177 Bacterial
9	1052.5	53.0	394	5	AAO21886	Aao21886 Isoprenoi
10	1045	52.6	398	5	AAO21878	Aao21878 Isoprenoi

No.	Score	Match	Length	DB	ID	Description
1	1985	100.0	394	1	PCT-US03-41812-18	Sequence 18, Appl
2	1985	100.0	394	24	US-09-941-947A-8	Sequence 8, Appli
3	1985	100.0	394	29	US-10-363-567-8	Sequence 8, Appli
4	1985	100.0	394	33	US-10-700-003-4	Sequence 4, Appli
5	1985	100.0	394	33	US-10-701-200-64	Sequence 64, Appl
6	1985	100.0	394	33	US-10-735-442-18	Sequence 18, Appl
7	1221.5	61.5	400	32	US-10-679-063-23144	Sequence 23144, A
8	1221.5	61.5	400	36	US-60-556-841-11593	Sequence 11593, A
9	1221.5	61.5	404	32	US-10-679-063-19465	Sequence 19465, A
10	1221.5	61.5	404	36	US-60-556-841-4537	Sequence 4537, Ap

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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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SUMMARIES

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3	1985	100.0	394	10	US-09-941-947A-8	Sequence 8, Appli
4	1985	100.0	394	15	US-10-700-003-4	Sequence 4, Appli
5	1985	100.0	394	15	US-10-363-567-8	Sequence 8, Appli
6	1985	100.0	394	17	US-10-735-442-18	Sequence 18, Appl
7	1215.5	61.2	396	14	US-10-381-779-117	Sequence 117, App
8	1052.5	53.0	394	14	US-10-381-779-119	Sequence 119, App

Handwritten notes:
 - Next to ID 64: 66689, 601
 - Next to ID 8: 3528 DP
 - Next to ID 8: chuk later
 - Next to ID 18: new case

Database : Issued_Patents_AA:*

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- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1985	100.0	394	4	US-09-934-903-4	Sequence 4, Appli	
2	1985	100.0	394	4	US-09-934-868-64	Sequence 64, Appl	
3	1215.5	61.2	617	4	US-09-252-991A-21113	Sequence 21113, A	
4	1114.5	56.1	398	4	US-09-328-352-7199	Sequence 7199, Ap	
5	1053	53.0	399	4	US-09-543-681A-6462	Sequence 6462, Ap	
6	1045	52.6	422	4	US-09-489-039A-12413	Sequence 12413, A	
7	962	48.5	435	4	US-09-540-236-2139	Sequence 2139, Ap	
8	818.5	41.2	399	3	US-09-491-362-7	Sequence 7, Appli	
9	818.5	41.2	399	4	US-09-874-562-7	Sequence 7, Appli	
10	818.5	41.2	406	4	US-09-959-509A-2	Sequence 2, Appli	
11	818.5	41.2	420	4	US-09-959-509A-4	Sequence 4, Appli	
12	818.5	41.2	477	3	US-09-449-335-6	Sequence 6, Appli	

-continued

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	485					

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<400> SEQUENCE: 81

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```

What is claimed is:

1. A pure isolate of a high growth methanotrophic bacterial strain which:

- (a) grows on a C1 carbon substrate selected from the group consisting of methane and methanol; and
- (b) comprises a functional Embden-Meyerhof carbon pathway, said pathway comprising a gene encoding a pyrophosphate dependent phosphofructokinase enzyme, the gene comprising an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO: 6.

2. A high growth methanotrophic bacterial strain according to claim 1 wherein the strain contains a functional Entner-Doudoroff carbon pathway.

3. A bacterial strain according to claim 1 having at least one gene encoding a fructose biphosphate aldolase enzyme.

4. A bacterial strain according to claim 3 wherein at least one gene encodes a fructose biphosphate aldolase enzyme having the amino acid sequence selected from the group consisting of SEQ ID NO: 16 and SEQ ID NO: 18.

5. The bacterial strain of claim 1 wherein the strain is a *Methylomonas* sp.

6. The bacterial strain of claim 5 having a 16s RNA profile as set forth in SEQ ID NO: 81.

7. The bacterial strain of claim 1 wherein, when the C1 carbon substrate is methanol, the strain produces glycogen comprising at least about 50% dry weight of biomass.

8. The bacterial strain of either claim 1 or claim 7 wherein the methanol concentration in the medium is about 2.5% (vol/vol).

9. The bacterial strain of any of claims 1 or 2 having a yield of greater than 1.0 grams of cell mass per gram of methane consumed.

10. The bacterial strain of any of claims 1 or 2 having a yield of greater than 0.5 grams of cell mass per gram of methane consumed.

11. The bacterial strain of any of claims 1 or 2 having a carbon conversion efficiency of greater than 40 g/mol methane/g/mol biomass.

12. The bacterial strain of any of claims 1 or 2 having a carbon conversion efficiency of greater than 64 g/mol methane/g/mol biomass.

13. A pure isolate of a high growth methanotrophic bacterial strain which grows on a C1 carbon substrate selected from the group consisting of methanol and methane, comprising the 16s RNA sequence as set forth in SEQ ID NO: 81 and having at least one gene encoding a pyrophosphate dependent Phosphofructokinase enzyme.

14. A pure isolate of a high growth methanotrophic bacterial strain having the ATCC designation PTA 2402.

* * * * *